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RAW SEQUENCE LISTING

DATE: 07/30/2001

PATENT APPLICATION: US/09/768,080

TIME: 15:09:22

Input Set : A:\GC527C3-seqlist.txt

Output Set: N:\CRF3\07302001\I768080.raw

3 <110> APPLICANT: Estell, David
 4 Harding, Fiona
 6 <120> TITLE OF INVENTION: PROTEINS PRODUCING AN ALTERED IMMUNOGENIC RESPONSE AND
 7 METHODS OF MAKING AND USING THE SAME
 9 <130> FILE REFERENCE: GC527C3
 11 <140> CURRENT APPLICATION NUMBER: US 09/768,080
 12 <141> CURRENT FILING DATE: 2001-01-23
 14 <150> PRIOR APPLICATION NUMBER: US 09/677,822
 15 <151> PRIOR FILING DATE: 2000-10-02
 17 <150> PRIOR APPLICATION NUMBER: US 09/500,135
 18 <151> PRIOR FILING DATE: 2000-02-08
 20 <150> PRIOR APPLICATION NUMBER: US 09/060,872
 21 <151> PRIOR FILING DATE: 1998-04-15
 23 <160> NUMBER OF SEQ ID NOS: 240
 25 <170> SOFTWARE: PatentIn Ver. 2.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1495
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Bacillus amyloliquefaciens
 32 <220> FEATURE:
 33 <221> NAME/KEY: mat_peptide
 34 <222> LOCATION: (417)..(1495)
 36 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 38 <222> LOCATION: (96)..(1244)
 40 <220> FEATURE:
 41 <221> NAME/KEY: misc_feature
 42 <222> LOCATION: (582)..(584)
 43 <223> OTHER INFORMATION: The nnn at positions 582 through 584 which in a
 44 preferred embodiment (aat) is to code for
 45 asparagine, but which may also code for proline.
 47 <220> FEATURE:
 48 <221> NAME/KEY: misc_feature
 49 <222> LOCATION: (585)..(587)
 50 <223> OTHER INFORMATION: The nnn at positions 585 through 587 which in a
 51 preferred embodiment (cct) is to code for proline,
 52 but which may also code for asparagine.
 54 <220> FEATURE:
 55 <221> NAME/KEY: misc_feature
 56 <222> LOCATION: (597)..(599)
 57 <223> OTHER INFORMATION: The nnn at positions 597 to 599 which in a
 58 preferred embodiment (aac) is to code for
 59 asparagine, but which may also code for aspartic acid.
 61 <220> FEATURE:
 62 <221> NAME/KEY: misc_feature
 63 <222> LOCATION: (678)..(680)
 64 <223> OTHER INFORMATION: The nnn at positions 678 through 680 which in a

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125 aaa tat att gtc ggg ttt aaa cag aca atg agc acg atg agc gcc gct 257
126 Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met Ser Ala Ala
127 -65 -60 -55
129 aag aag aaa gat gtc att tot gaa aaa ggc ggg aaa gtg caa aag caa 305
130 Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly Lys Val Gln Lys Gln
131 -50 -45 -40
133 ttc aaa tat gta gac gca gct tca gct aca tta aac gaa aaa gct gta 353
134 Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr Leu Asn Glu Lys Ala Val
135 -35 -30 -25
137 aaa gaa ttg aaa aaa gac cgg agc gtc gct tac gtt gaa gaa gat cac 401
138 Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His
139 -20 -15 -10
141 gta gca cat gcg tac gcg cag tcc gtg cct tac ggc gta tca caa att 449
142 Val Ala His Ala Tyr Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile
143 -5 -1 1 5 10
145 aaa gcc cct gct ctg cac tct caa ggc tac act gga tca aat gtt aaa 497
146 Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys
147 15 20 25
149 gta gcg gtt atc gac agc ggt atc gat tot tct cat cct gat tta aag 545
150 Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys
151 30 35 40
W--> 153 gta gca ggc gga gcc agc atg gtt cct tct gaa aca nnn nnn ttc caa 593
W--> 154 Val Ala Gly Gly Ala Ser Met Val Pro Ser Glu Thr Xaa Xaa Phe Gln
155 45 50 55
W--> 157 gac nnn aac tct cac gga act cac gtt gcc ggc aca gtt gcg gct ctt 641
W--> 158 Asp Xaa Asn Ser His Gly Thr His Val Ala Gly Thr Val Ala Ala Leu
159 60 65 70 75
W--> 161 aat aac tca atc ggt gta tta ggc gtt gcg cca agc nnn nnn ctt tac 689
W--> 162 Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser Xaa Xaa Leu Tyr
163 80 85 90
W--> 165 gct gta aaa gtt ctc ggt nnn nnn ggt tcc ggc caa tac agc tgg atc 737
W--> 166 Ala Val Lys Val Leu Gly Xaa Xaa Gly Ser Gly Gln Tyr Ser Trp Ile
167 95 100 105
169 att aac gga atc gag tgg gcg atc gca aac aat atg gac gtt att aac 785
170 Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn
171 110 115 120
173 atg agc ctc ggc gga cct tct ggt tct gct gct tta aaa gcg gca gtt 833
174 Met Ser Leu Gly Gly Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val
175 125 130 135
177 gat aaa gcc gtt gca tcc ggc gtc gta gtc gtt gcg gca gcc ggt aac 881
178 Asp Lys Ala Val Ala Ser Gly Val Val Val Ala Ala Ala Gly Asn
179 140 145 150 155
W--> 181 gaa ggc nnn nnn ggc agc tca agc aca gtg ggc tac cct ggt aaa tac 929
W--> 182 Glu Gly Xaa Xaa Gly Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr
183 160 165 170
185 cct tct gtc att gca gta ggc gct gtt gac agc agc aac caa aga gca 977
186 Pro Ser Val Ile Ala Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala
187 175 180 185
189 tct ttc tca agc gta gga cct gag ctt gat gtc atg gca cct ggc gta 1025

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65     preferred embodiment (gca) is to code for
66     alanine, but which may also code for serine.
68 <220> FEATURE:
69 <221> NAME/KEY: misc_feature
70 <222> LOCATION: (681)..(683)
71 <223> OTHER INFORMATION: The nnn at positions 681 through 683 which in a
72     preferred embodiment (tca) is to code for serine,
73     but which may also code for alanine.
75 <220> FEATURE:
76 <221> NAME/KEY: misc_feature
77 <222> LOCATION: (708)..(710)
78 <223> OTHER INFORMATION: The nnn at positions 708 through 710 which in a
79     preferred embodiment (gct) is to code for
80     alanine, but which may also code for aspartic acid.
82 <220> FEATURE:
83 <221> NAME/KEY: misc_feature
84 <222> LOCATION: (711)..(713)
85 <223> OTHER INFORMATION: The nnn at positions 711 through 713 which in a
86     preferred embodiment (gac) is to code for
87     aspartic acid, but which may also code for alanine.
89 <220> FEATURE:
90 <221> NAME/KEY: misc_feature
91 <222> LOCATION: (888)..(890)
92 <223> OTHER INFORMATION: The nnn at positions 888 through 890 which in a
93     preferred embodiment (act) is to code for
94     threonine, but which may also code for serine.
96 <220> FEATURE:
97 <221> NAME/KEY: misc_feature
98 <222> LOCATION: (891)..(893)
99 <223> OTHER INFORMATION: The nnn at positions 891 through 893 which in a
100     preferred embodiment (tcc) is to code for
101     serine, but which may also code for threonine.
103 <220> FEATURE:
104 <221> NAME/KEY: misc_feature
105 <222> LOCATION: (1167)..(1169)
106 <223> OTHER INFORMATION: The nnn at positions 1167 through 1169 which in
107     a preferred embodiment (gaa) is to code for
108     glutamic acid, but which may also code for glutamine.
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111 ggtctactaa aatattattc catactatac aattaataca cagaataatc tgtctattgg 60
113 ttattctgca aatgaaaaaa aggagaggat aaaga atg aga ggc aaa aaa gta 113
114                                     Met Arg Gly Lys Lys Val
115                                     -105
117 tqg atc agt ttg ctg ttt gct tta gcg tta atc ttt acg atg gcg ttc 161
118 Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu Ile Phe Thr Met Ala Phe
119 -100 -95 -90
121 ggc agc aca tcc tct gcc cag gcg gca ggg aaa tca aac ggg gaa aag 209
122 Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly Lys Ser Asn Gly Glu Lys
123 -85 -80 -75 -70

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190 Ser Phe Ser Ser Val Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val
191          190          195          200
193 tct atc caa agc acg ctt cct gga aac aaa tac ggg gcg tac aac ggt 1073
194 Ser Ile Gln Ser Thr Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly
195          205          210          215
197 acg tca atg gca tct ccg cac gtt gcc gga gcg get get ttg att ctt 1121
198 Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu
199 220          225          230          235
W--> 201 tct aag cac ccg aac tgg aca aac act caa gtc cgc agc agt tta hnn 1169
W--> 202 Ser Lys His Pro Asn Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Xaa
203          240          245          250
205 aac acc act aca aaa ctt ggt gat tct ttc tac tat gga aaa ggg ctg 1217
206 Asn Thr Thr Thr Lys Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu
207          255          260          265
209 atc aac gta cag gcg gca get cag taa aacataaaaa accggccttg 1264
210 Ile Asn Val Gln Ala Ala Ala Gln
211          270          275
213 gcccgccggg ttttttttatt ttttttcttc cgcattgttca atccgctcca taatcgacgg 1324
215 atggctccct ctgaaaaatt taacgagaaa cggcggggttg acccggtcca gtcccgtaac 1384
217 gcccaagtc tgaaacgtct caategcgc ttcccggttt ccggtcagct caatgcgcta 1444
219 acggtcggcg gcgttttctt gataccggga gacggcattc gtaatcggtat c 1495
222 <210> SEQ ID NO: 2
223 <211> LENGTH: 382
224 <212> TYPE: PRT
225 <213> ORGANISM: Bacillus amyloliquefaciens
227 <220> FEATURE:
228 <221> NAME/KEY: VARIANT
229 <222> LOCATION: (163)...(163)
230 <223> OTHER INFORMATION: Xaa = Asn or Pro
232 <220> FEATURE:
233 <221> NAME/KEY: VARIANT
234 <222> LOCATION: (164)...(164)
235 <223> OTHER INFORMATION: Xaa = Pro or Asn
237 <220> FEATURE:
238 <221> NAME/KEY: VARIANT
239 <222> LOCATION: (167)...(167)
240 <223> OTHER INFORMATION: Xaa = Asn or Asp
242 <220> FEATURE:
243 <221> NAME/KEY: VARIANT
244 <222> LOCATION: (195)...(195)
245 <223> OTHER INFORMATION: Xaa = Ala or Ser
247 <220> FEATURE:
248 <221> NAME/KEY: VARIANT
249 <222> LOCATION: (196)...(196)
250 <223> OTHER INFORMATION: Xaa = Ser or Ala
252 <220> FEATURE:
253 <221> NAME/KEY: VARIANT
254 <222> LOCATION: (205)...(205)
255 <223> OTHER INFORMATION: Xaa = Ala or Asp

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257 <220> FEATURE:
258 <221> NAME/KEY: VARIANT
259 <222> LOCATION: (206)...(206)
260 <223> OTHER INFORMATION: Xaa = Asp or Ala
262 <220> FEATURE:
263 <221> NAME/KEY: VARIANT
264 <222> LOCATION: (265)...(265)
265 <223> OTHER INFORMATION: Xaa = Thr or Ser
267 <220> FEATURE:
268 <221> NAME/KEY: VARIANT
269 <222> LOCATION: (266)...(266)
270 <223> OTHER INFORMATION: Xaa = Ser or Thr
272 <220> FEATURE:
273 <221> NAME/KEY: VARIANT
274 <222> LOCATION: (358)...(358)
275 <223> OTHER INFORMATION: Xaa = Gln or Glu
277 <400> SEQUENCE: 2
278 Met Arg Gly Lys Lys Val Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu
279      1              5              10              15
280 Ile Phe Thr Met Ala Phe Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly
281      20              25              30
282 Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met
283      35              40              45
284 Ser Thr Met Ser Ala Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly
285      50              55              60
286 Gly Lys Val Gln Lys Gln Phe Lys Tyr Val Asp Ala Ala Ser Ala Thr
287      65              70              75              80
288 Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala
289      85              90              95
290 Tyr Val Glu Glu Asp His Val Ala His Ala Tyr Ala Gln Ser Val Pro
291      100             105             110
292 Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr
293      115             120             125
294 Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser
295      130             135             140
296 Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala Ser Met Val Pro Ser
297      145             150             155             160
W--> 298 Glu Thr Xaa Xaa Phe Gln Asp Xaa Asn Ser His Gly Thr His Val Ala
299      165             170             175
300 Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala
301      180             185             190
W--> 302 Pro Ser Xaa Xaa Leu Tyr Ala Val Lys Val Leu Gly Xaa Xaa Gly Ser
303      195             200             205
304 Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn
305      210             215             220
306 Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Ala
307      225             230             235             240
308 Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala Ser Gly Val Val Val
309      245             250             255

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VERIFICATION SUMMARY

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Input Set : A:\GC527C3-seqlist.txt

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L:153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2